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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: Mon Aug 13 15:16:20 EDT 2007

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Application No: 10576807

Version No: 1.1

Input Set:

Output Set:

Started: 2007-08-13 15:15:47.946

Finished: 2007-08-13 15:15:48.651

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 705 ms

Total Warnings: 10

Total Errors: 0

No. of SeqIDs Defined: 12

Actual SeqID Count: 12

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (10)
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SEQUENCE LISTING

<110> Clark, Janet

<120> METHOD FOR IDENTIFYING COMPOUNDS THAT
AFFECT EXPRESSION OF TRYPTOPHAN HYDROXYLASE ISOFORM 2

<130> 21487YP

<140> 10/576,807

<141> 2006-04-21

<150> PCT/US2004/34619

<151> 2004-10-20

<150> 60/514,268

<151> 2003-10-24

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 447

<212> PRT

<213> Mus musculus

<400> 1

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			20					25					30		
Gly	Leu	Ile	Lys	Val	Leu	Lys	Ile	Phe	Gln	Glu	Asn	His	Val	Ser	Leu
		35					40					45			
Leu	His	Ile	Glu	Ser	Arg	Lys	Ser	Lys	Gln	Arg	Asn	Ser	Glu	Phe	Glu
		50				55					60				
Ile	Phe	Val	Asp	Cys	Asp	Ile	Ser	Arg	Glu	Gln	Leu	Asn	Asp	Ile	Phe
65				70					75					80	
Pro	Leu	Leu	Lys	Ser	His	Ala	Thr	Val	Leu	Ser	Val	Asp	Ser	Pro	Asp
			85						90				95		
Gln	Leu	Thr	Ala	Lys	Glu	Asp	Val	Met	Glu	Thr	Val	Pro	Trp	Phe	Pro
			100					105				110			
Lys	Lys	Ile	Ser	Asp	Leu	Asp	Phe	Cys	Ala	Asn	Arg	Val	Leu	Leu	Tyr
		115					120					125			
Gly	Ser	Glu	Leu	Asp	Ala	Asp	His	Pro	Gly	Phe	Lys	Asp	Asn	Val	Tyr
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145				150					155					160	
Gly	Asp	Pro	Ile	Pro	Lys	Ile	Glu	Phe	Thr	Glu	Glu	Glu	Ile	Lys	Thr
			165					170					175		
Trp	Gly	Thr	Ile	Phe	Arg	Glu	Leu	Asn	Lys	Leu	Tyr	Pro	Thr	His	Ala
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Cys	Arg	Glu	Tyr	Leu	Arg	Asn	Leu	Pro	Leu	Leu	Ser	Lys	Tyr	Cys	Gly
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Tyr	Arg	Glu	Asp	Asn	Ile	Pro	Gln	Leu	Glu	Asp	Val	Ser	Asn	Phe	Leu
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Lys Glu Arg Thr Gly Phe Ser Ile Arg Pro Val Ala Gly Tyr Leu Ser
 225 230 235 240
 Pro Arg Asp Phe Leu Ser Gly Leu Ala Phe Arg Val Phe His Cys Thr
 245 250 255
 Gln Tyr Val Arg His Ser Ser Asp Pro Leu Tyr Thr Pro Glu Pro Asp
 260 265 270
 Thr Cys His Glu Leu Leu Gly His Val Pro Leu Leu Ala Glu Pro Ser
 275 280 285
 Phe Ala Gln Phe Ser Gln Glu Ile Gly Leu Ala Ser Leu Gly Ala Ser
 290 295 300
 Glu Glu Thr Val Gln Lys Leu Ala Thr Cys Tyr Phe Phe Thr Val Glu
 305 310 315 320
 Phe Gly Leu Cys Lys Gln Asp Gly Gln Leu Arg Val Phe Gly Ala Gly
 325 330 335
 Leu Leu Ser Ser Ile Ser Glu Leu Lys His Ala Leu Ser Gly His Ala
 340 345 350
 Lys Val Lys Pro Phe Asp Pro Lys Ile Ala Cys Lys Gln Glu Cys Leu
 355 360 365
 Ile Thr Ser Phe Gln Asp Val Tyr Phe Val Ser Glu Ser Phe Glu Asp
 370 375 380
 Ala Lys Glu Lys Met Arg Glu Phe Ala Lys Thr Val Lys Arg Pro Phe
 385 390 395 400
 Gly Leu Lys Tyr Asn Pro Tyr Thr Gln Ser Val Gln Val Leu Arg Asp
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<211> 488

<212> PRT

<213> Mus musculus

<400> 2

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 Ser Leu Thr Gln Asn Lys Ala Ile Lys Ser Glu Asp Lys Lys Ser Gly
 35 40 45
 Lys Glu Pro Gly Lys Gly Asp Thr Thr Glu Ser Ser Lys Thr Ala Val
 50 55 60
 Val Phe Ser Leu Lys Asn Glu Val Gly Gly Leu Val Lys Ala Leu Arg
 65 70 75 80
 Leu Phe Gln Glu Lys His Val Asn Met Leu His Ile Glu Ser Arg Arg
 85 90 95
 Ser Arg Arg Arg Ser Ser Glu Val Glu Ile Phe Val Asp Cys Glu Cys
 100 105 110
 Gly Lys Thr Glu Phe Asn Glu Leu Ile Gln Leu Leu Lys Phe Gln Thr
 115 120 125
 Thr Ile Val Thr Leu Asn Pro Pro Glu Ser Ile Trp Thr Glu Glu Glu
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<213> Artificial Sequence

<220>
<223> TPH2b riboprobe

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gaattcaatg agctcatcca gttgctgaaa tttagacca ccattgtgac cctgaatccg 180
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<212> DNA
<213> Artificial Sequence

<220>
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aaaagcgagg acaagaaaag cggcaaagag cccggcaaag gcgacaccac agagagcagc 180
aagacagcag ttgtgttttc cttgaagaat gaagttgggtg ggctggtgaa agcacttaga 240
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agtttctaagt cgaaatcttc gtggactgcg aatgtggcaa aacggaattc aatgagctca 360
tccagttgct gaaatttcag accaccattg tgaccctgaa tccgcctgag agcatttgga 420
cggaggaaga agatctcgag gatgtgccgt ggttccctcg gaagatctct gagttagaca 480
gatgctctca ccgagtcctc atgtacggca ccgagcttga tgccgaccat ccaggattta 540
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tgttccggga gctctccaaa ctctaccgca ctcatgcttg ccgggagtac ctgaaaaacc 720
tccccctgct gaccaagtac tgtggctaca gggaagacaa cgtgccgcaa ctggaagacg 780
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<220>
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ggctatcggg aagacaacat cccgcaactg gaggatgtct ccaacttttt aaaagaacgc 180
actgggtttt ccatcgttc tgtggctggg tacctctcac cgagagattt tctgtcgggg 240
ttagectttc gagtctttca ctgcactcag tatgtgagac acagttcaga tcccccttac 300
actccagagc cagacacctg ccatgaactc ctaggccacg ttctctctct ggctgaaccc 360
agttttgcct aattctccca agaaattggc ctggcttccc ttggagcttc agaggagaca 420
gttcaaaaac tggcaacgtg ctactttttc actgtggagt ttgggctgtg caaacaagat 480
ggacagctga gagtctttgg ggccggcttg ctttcttcca tcagtgaact caaacatgca 540
ctttctggac atgccaaagt caagcccttt gatcccaaga ttgcctgtaa acaggaatgt 600

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ctcatcacga gcttccagga tgtctacttt gtatctgaga gctttgaaga tgcaaaggag 660
aagatgagag aatttgccaa gaccgtgaag cgcctgttg gactgaagta caaccgtac 720
acacagagtg ttcaggttct cagagacacc aagagcataa ctagtgccat gaatgagttg 780
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<211> 22
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<223> Murine TPH2 probe mTPH2-1292T

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